

09881050 11301
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1201	a					

Figure 1

MIKHFFGTVLVLLASTTIFSLDLKLIIFQQRQVNQESLKLLNKLQTL~~SIQQ~~CLPH
RKNFLLPQKSLSPQQYQKGHTLAILHEMLQQIFSLFRANISLDGWEENHTEK
FLIQLHQQLEYLEALMGLEAEKLSGTLGSDNRLRLQVKMYFRRIHDYLENQD
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Figure 2

09881050 111301

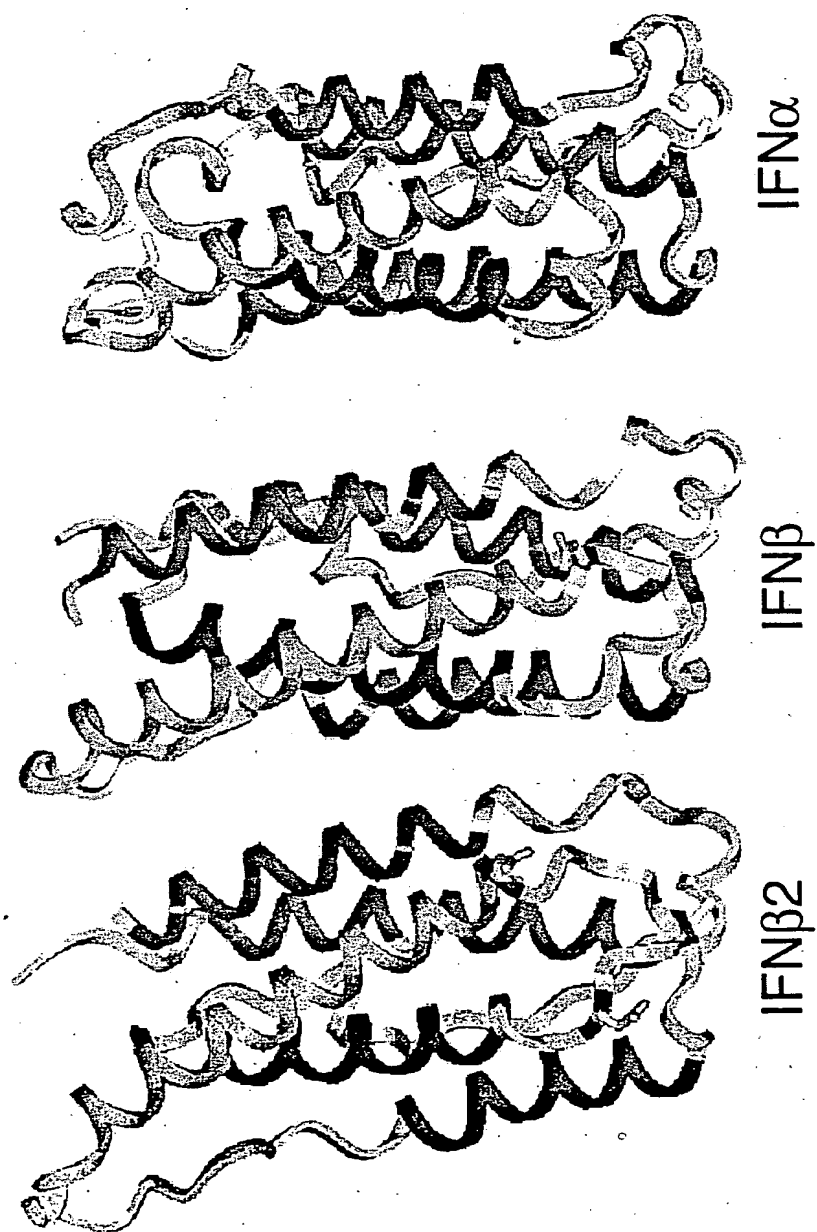
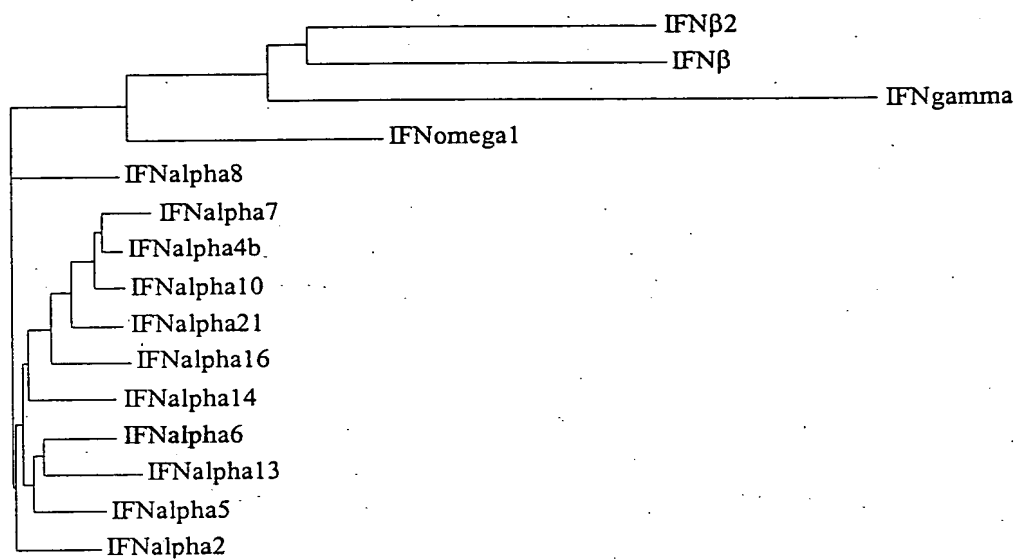


Figure 3

	1		70
IFNB2	(1)	MILKHFPGTVLVLLASTIFSLDLKEIIFQOROVNOESEKLLNKLO-TLSIQOCLPHRKNEFLLPOKSLSP	
IFNB	(1)	MTNKCLOLALLCFSTALSMYNLLGFLORSSNFQCKLLWOLNGRIEY--CLKORMNEDIPEEIKQL	
IFNalpha8	(1)	MALTFYLLVALVVLVSYSKSFSSLGCDLPOTHS-LGNRRALILLAQMR-RISPFSCCLKDRHDFEPQEEFDD	
IFNalpha7	(1)	MARSFSLLMVVLVSYSKISCSLGCDLPOTHS-LRNRRALILLAQMG-RISPFSCCLKDRHEERFPPEEFDG	
IFNalpha6	(1)	MALPFALLMALVVLSCSSCSLDCDLPOTHS-LGHRRTMMLLAQMR-RISLFSCLKDRHDFEPQEEFDG	
IFNalpha5	(1)	MALPFVLLMALVVLNCKSICSLGCDLPOTHS-LSNRRTLMLMAQMG-RISPFSCCLKDRHDFEPQEEFDG	
IFNalpha4b	(1)	MALSFSLLMAVLVLSYKISCSLGCDLPOTHS-LGNRRALILLAQMG-RISPFSCCLKDRHDFEPQEEFDG	
IFNalpha21	(1)	MALSFSLLMAVLVLSYKISCSLGCDLPOTHS-LGNRRALILLAQMG-RISPFSCCLKDRHDFEPQEEFDG	
IFNalpha2	(1)	MALTFALLVALLVLSCKSSCSVGCGLDPOTHS-LGSRRTLMLLAQMR-RISLFSCLKDRHDFEPQEEF-G	
IFNalpha16	(1)	MALSFSLLMAVLVLSYKISCSLGCDLPOTHS-LGNRRALILLAQMG-RISHFSCLKDRYDFGFPQEEVFDG	
IFNalpha14	(1)	MALPFALLMALVVLSCSSCSLGCNLSOTHS-LNNRRTLMLMAQMR-RISPFSCCLKDRHDFEPQEEFDG	
IFNalpha13	(1)	MASPEALLMVLVLSCKSSCSLGCDLPOTHS-LDNRRTLMLLAQMS-RISPFSCCLKDRHDFEPQEEFDG	
IFNalpha10	(1)	MALSFSLLMAVLVLSYKISCSLGCDLPOTHS-LGNRRALILLGQMG-RISPFSCCLKDRHDFEPQEEFDG	
IFNomega1	(1)	MALLEPLLAALVMTSYSPVGS LGCDLPQNHG-LLSRNTLVLLHQM-RISPCLCLKDRHDFEPQEEVKG	
IFNgamma	(1)	MKYT-SYLLAFQCLVILGSLGCYCODEYVKE---AENLKKYFNAG---H--SDVADNGTLE--LGILK	
Consensus	(1)	MAL F LLMALLVLS KS CSLGCDLPOTHS L NRR L LLAQM RISPFSCCLKDRHDFEPQEEFDG	140
	71		
IFNB2	(70)	QOYQKGHTEALHEMLQOIFSLFRANISLDGWEENHTEKFLIOLHQOLEVLEALMGLAEKLSGTUGSDN	
IFNB	(69)	QOFQKEDAALETVEMLQNIFAIFRODSSSTGWNETIVENLLANVHOINHLKTVLEEKLEKEDFTRGKLM	
IFNalpha8	(69)	QOFQKQAISVLHEMIQOTFNLFSTKDSSAALDETLLDEFYIELDQOLNDLESCVMQEVGVIESPLMYED	
IFNalpha7	(69)	HOFOKTOAISVLHEMIQOTFNLFSTEDSSAAWEQSLLEKEFSTELYQOLNDLEACVIOEVGVEETPLMNED	
IFNalpha6	(69)	NQFQKAEAISVLHEVIQOTFNLFSTKDSSVADDERLLDKLYTELYQOLNDLEACVMQEVVVGGTPLMNED	
IFNalpha5	(69)	NQFQKQAISVLHEMIQOTFNLFSTKDSSATWDETLLDKFYTELYQOLNDLEACMMQEVGVEDTPLMNVD	
IFNalpha4b	(69)	HOFOKTOAISVLHEMIQOTFNLFSTEDSSAAWEQSLLEKEFSTELYQOLNDLEACVIOEVGVEETPLMNVD	
IFNalpha21	(69)	NQFQKQAISVLHEMIQOTFNLFSTKDSSATWDETLLDKFYTELYQOLNDLEACVIOEVGVEETPLMNVD	
IFNalpha2	(68)	NQFQKAETIPVLHEMIQOIFNLFSTKDSSAAWDETLLDKFYTELYQOLNDLEACVIOGVGVETETPLMKED	
IFNalpha16	(69)	NQFQKQAISAFHEMIQOTFNLFSTKDSSAAWDETLLDKFYTELYQOLNDLEACVTOEVGVVEETPLMNED	
IFNalpha14	(69)	NQFQKQAISVLHEMIQOTFNLFSTKNSSAAWDETLLDKFYTELYQOLNDLEACVIOEVGVEETPLMNED	
IFNalpha13	(69)	NQFQKAPATSVLHEMIQOIFNLFSTKDSSAAWDETLLDKFYTELYQOLNDLEACVIOEVGVEETPLMNED	
IFNalpha10	(69)	NQFQKQAISVLHEMIQOTFNLFSTEDSSAAWEQSLLEKEFSTELYQOLNDLEACVIOEVGVEETPLMNED	
IFNomega1	(69)	SOLQKAHVMSVLHEMLQOIFSLFHTERSAAWNMTLLDQLHTGLHQOLQHLETCLLOVVGEGESAGAISS	
IFNgamma	(58)	NWKEESDRKIMQSQIVSFYFKLFKNFKD---DQS-FOKSVETIKEDMN-VKFFNSNKKKRDDFEKJITNY	
Consensus	(71)	NQFQKQAISVLHEMIQOTFNLFSTKDSSAAWE LLDKF TELYQOLNDLEACV QEVGVEETPLMN D	210
	141		
IFNB2	(140)	LRLQVKMYFRRIHIDYLE-NQDYSTCAWATVQVEISRCLFFVFSLTEKLSKQGRPLNDMKQELTTEFRSPR	
IFNB	(139)	SSLHTKRYGRILHYLK-AKEYSHCAWTVRVEILRNEYFINRLTGILRN-----	
IFNalpha8	(139)	SILAVRKYFORITLYLT-EKKYSSCAWEVVRAEIMRSFSLINLOKRLKSKE-----	
IFNalpha7	(139)	FILAVRKYFORITLYLM-EKKYSPCAWEVVRAEIMRSFSFSTNLKKGLRRKD-----	
IFNalpha6	(139)	SILAVRKYFORITLYLT-EKKYSPCAWEVVRAEIMRSFSSSRNLOERLRRKE-----	
IFNalpha5	(139)	SILTVRKYFORITLYLT-EKKYSPCAWEVVRAEIMRSFSLSANLOERLRRKE-----	
IFNalpha4b	(139)	SILAVRKYFORITLYLT-EKKYSPCAWEVVRAEIMRSLSFSTNLQKRLRRKD-----	
IFNalpha21	(139)	SILAVKKYFORITLYLT-EKKYSPCAWEVVRAEIMRSFSLSKIFOERLRRKE-----	
IFNalpha2	(138)	SILAVRKYFORITLYLK-EKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKE-----	
IFNalpha16	(139)	SILAVRKYFORITLYLM-GKKYSPCAWEVVRAEIMRSFSFSTNLQKGLRRKD-----	
IFNalpha14	(139)	SILAVKKYFORITLYLM-EKKYSPCAWEVVRAEIMRSFSFSTNLQKRLRRKD-----	
IFNalpha13	(139)	SILAVKKYFRRITLYLT-EKKYSPCAWEVVRAEIMRSLSLSTNLQERLRRKE-----	
IFNalpha10	(139)	SILAVRKYFORITLYLI-ERKYSPCAWEVVRAEIMRSLSFSTNLQKRLRRKD-----	
IFNomega1	(139)	PALTIRRYFOGIRVYLYK-EKKYSDCAWEVVRAEIMKSLFLSTNMQERLRSKDRDLGSS-----	
IFNgamma	(122)	SVTDLNVORKAIELHTQVMAELSPAAKTGKR---KRSQML---FRGRRASQ-----	
Consensus	(141)	SILAVRKYFORITLYL EKKYSPCAWEVVRAEIMRSFS STNLQ RLRRK	

Figure 4

Protein Level Comparison



Nucleotide Level Comparison

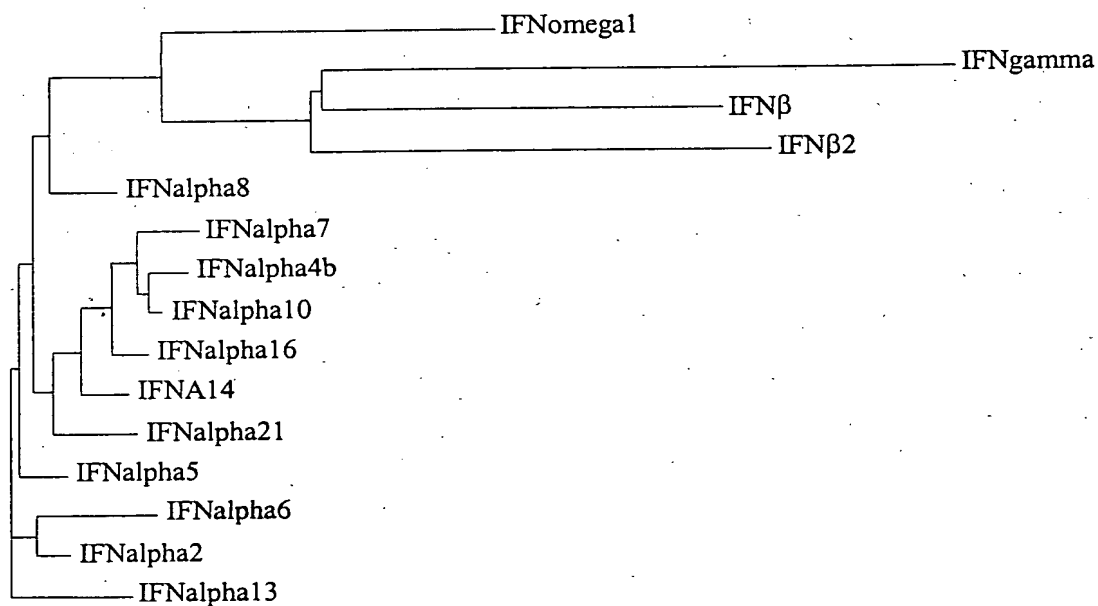


Figure 5

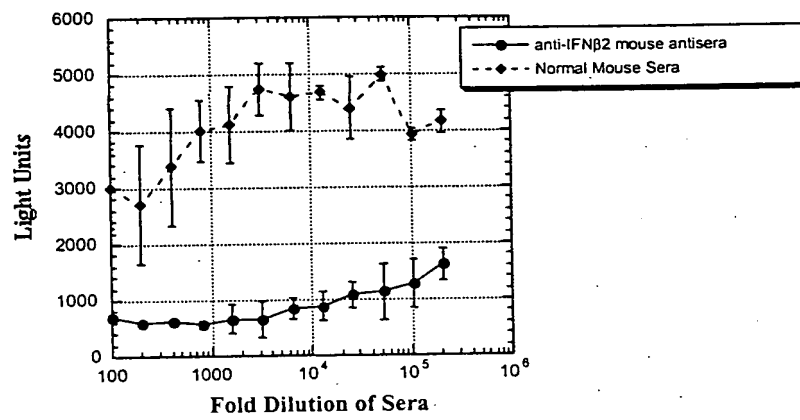


Figure 7

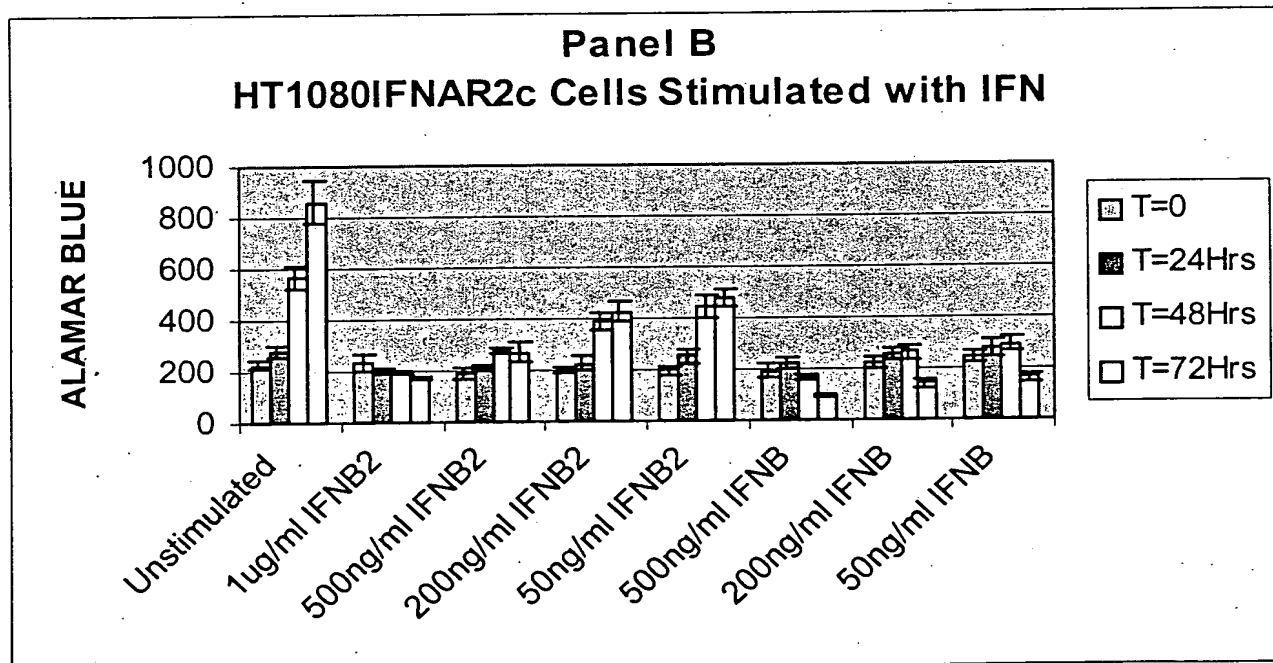
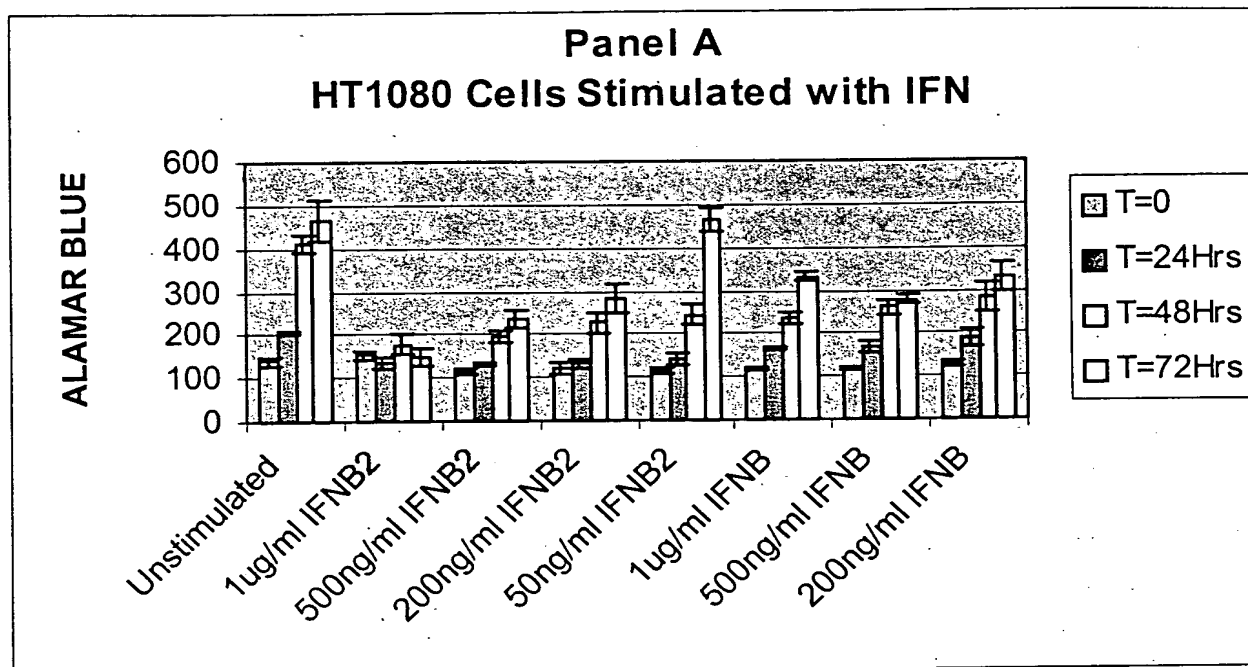


Figure 8

09881050-111301

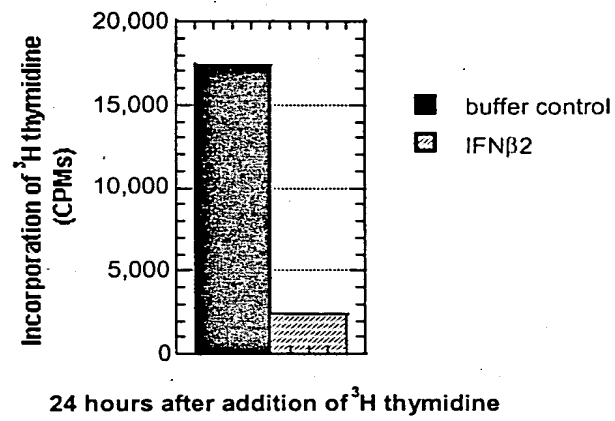


Figure 9

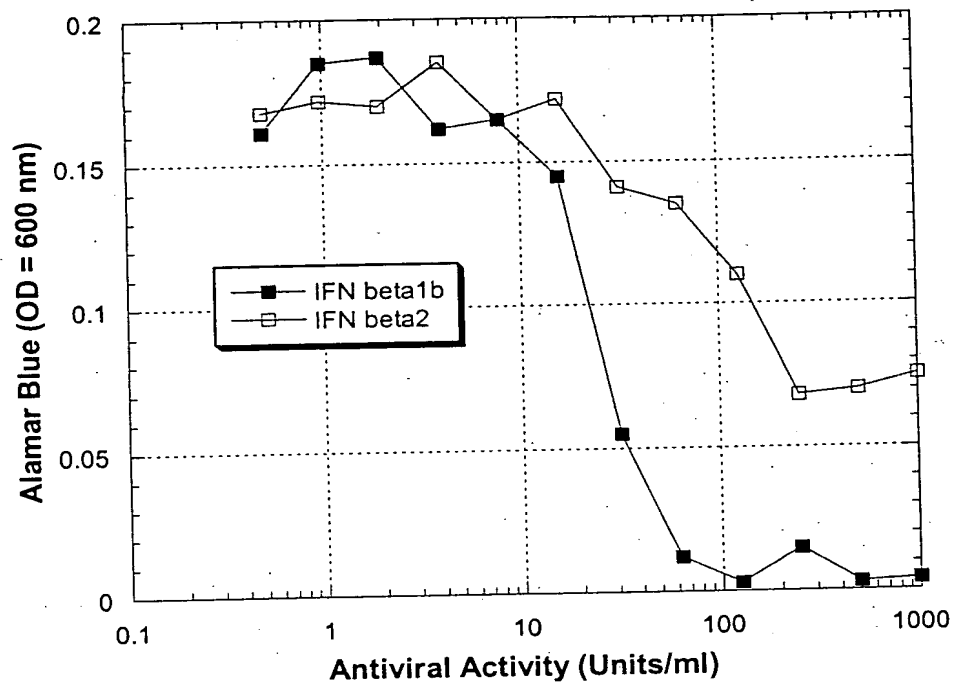


Figure 10

09881050 "11301

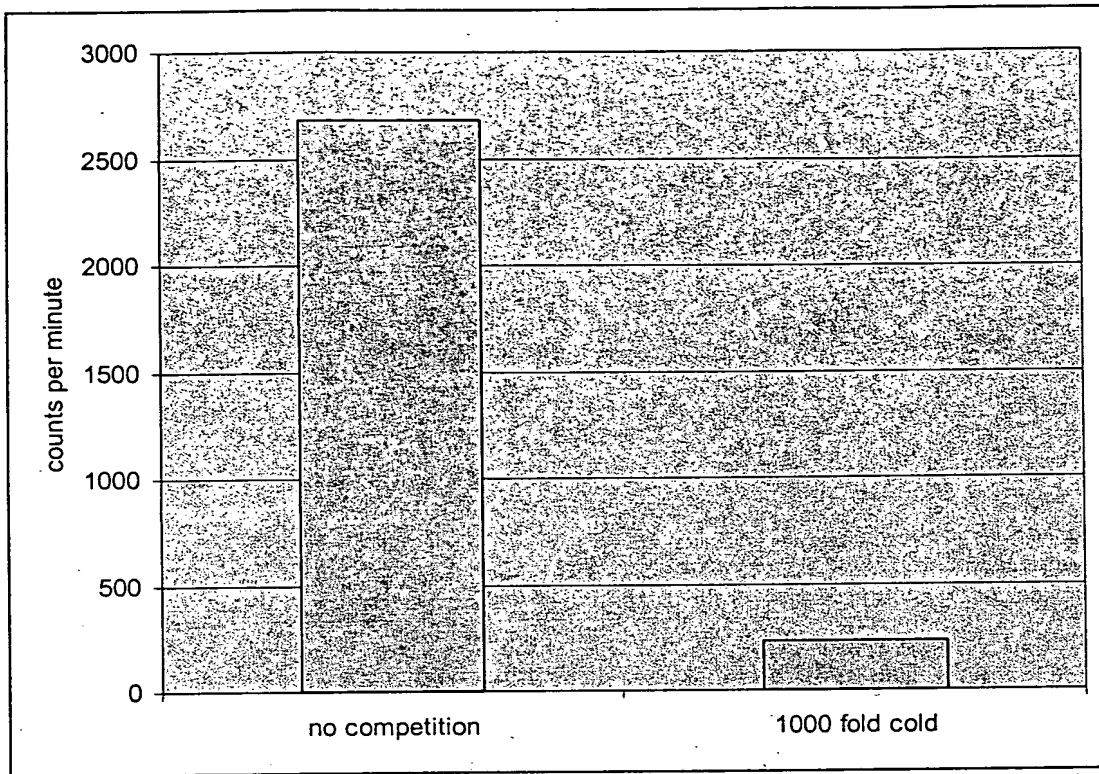


Figure 11

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121	aattgcctca	aggaaagcat	acaatgaata	agttattttg	gtacttcctc	aaaatagcca
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301	caaaataatc	tgagatgcat	gaaaggcaaa	cattcactag	agctggaatt	tcctaagtc
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Figure 12

09631050 "11301"

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541 aattcagcag tgtctaccac acaggaaaaa ctttctgctt cctcagaagt ctttgagtcc
601 ttaactgtac caaaaaggac acactctggc cattcttcat gagatgct

Figure 13

09881050-111301

MIKHFFGTVLVLLASTTIFSLDLKLIIFQQRQVNQESLKLLNKLQTL^{SIQ}
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Figure 14

0981050.11301
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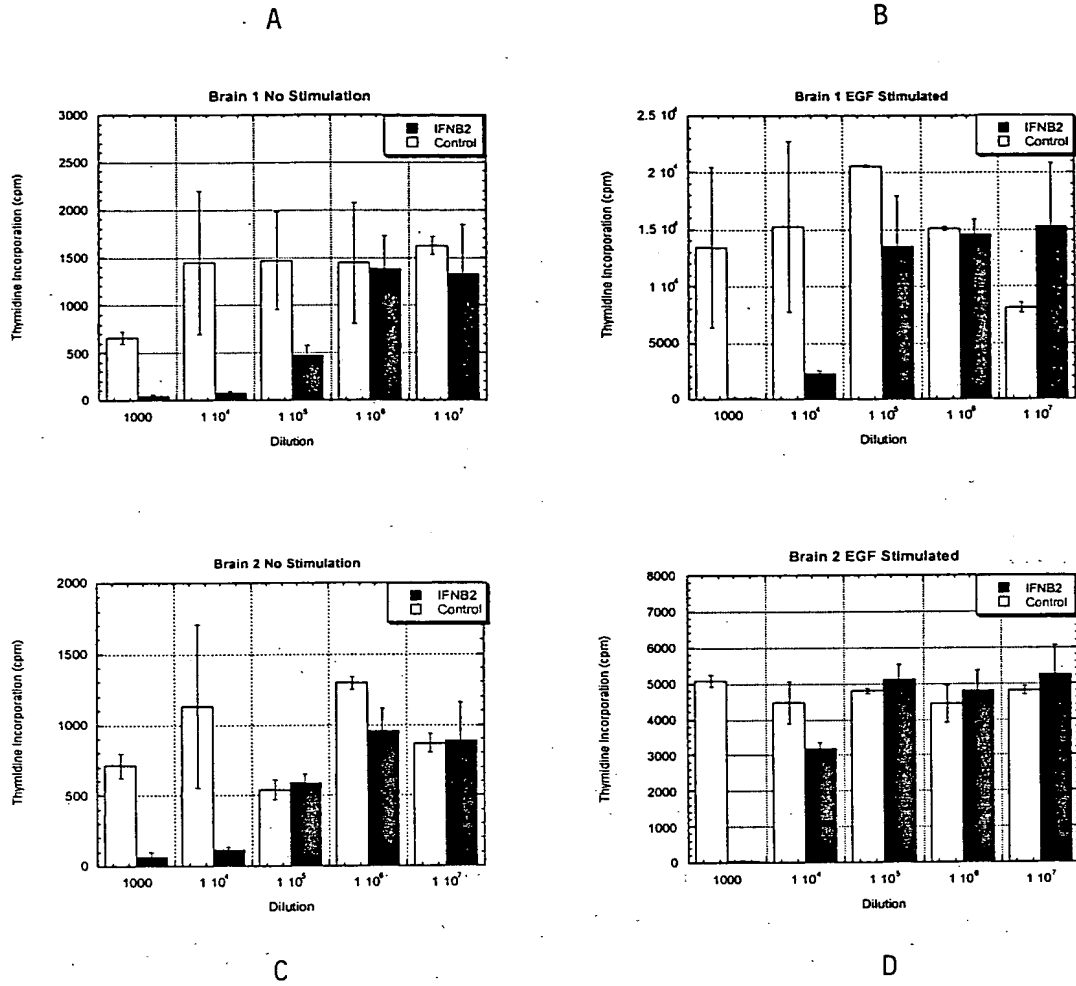


Figure 15